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JUN 21 2001  
TECH CENTER 1600/2500  
1651

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/715,909

DATE: 05/15/2001  
TIME: 11:31:45

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\05152001\I715909.raw

ENTERED

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4 <110> APPLICANT: Flannagan, Ronald D.
5      Mathis, John P.
6      Meyer, Terry E.
9 <120> TITLE OF INVENTION: Novel Bt Toxin Receptors From
10     Lepidopteran Insects and Methods of Use
13 <130> FILE REFERENCE: 35718/204664
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/715,909
C--> 15 <141> CURRENT FILING DATE: 2000-11-17
15 <150> PRIOR APPLICATION NUMBER: 60/166,285
16 <151> PRIOR FILING DATE: 1999-11-18
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5498 .
24 <212> TYPE: DNA
25 <213> ORGANISM: Ostrinia nubilalis
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (162)...(5312)
31 <400> SEQUENCE: 1
32 cataataaca ataaagagga agtgtgtgtg aaaaacgaag aagttaataa acctggataa      60
33 ttaaacctga aaaaaaccgg ttttaagtgc gaattttgc tgaaggacaa ccgtggataa      120
34 gctcaaatat taaaattcta cataactaag gatcatgcaa a atg ggg gtt gag agg      176
35                                         Met Gly Val Glu Arg
36                                         1             5
38 ttc ttc cca gca gtg cta ctg gtc tct tta gcc tct gcc gca cta gcc      224
39 Phe Phe Pro Ala Val Leu Leu Val Ser Leu Ala Ser Ala Ala Leu Ala
40           10          15          20
42 aac caa cga tgt tac att atc gca ata cca aga ccg gag act ccg      272
43 Asn Gln Arg Cys Ser Tyr Ile Ile Ala Ile Pro Arg Pro Glu Thr Pro
44           25          30          35
46 gaa ctg ccg cct att gat tac gaa gga aaa tca tgg agt gaa cag cct      320
47 Glu Leu Pro Pro Ile Asp Tyr Glu Gly Lys Ser Trp Ser Glu Gln Pro
48           40          45          50
50 cta ata ccc ggc ccg acc cga gag gaa gta tgt atg gag aac ttc tta      368
51 Leu Ile Pro Gly Pro Thr Arg Glu Glu Val Cys Met Glu Asn Phe Leu
52           55          60          65
54 ccg gat caa atg att cag gtc ata tac atg gag gaa gaa atc gaa gga      416
55 Pro Asp Gln Met Ile Gln Val Ile Tyr Met Glu Glu Glu Ile Glu Gly
56   70          75          80          85
58 gac gtc atc att gcg aag ctt aac tat caa ggg tcc aac acg ccg gtg      464
59 Asp Val Ile Ile Ala Lys Leu Asn Tyr Gln Gly Ser Asn Thr Pro Val
60           90          95          100
62 ctg tcg att atg tca ggc cag ccc aga gcc cag ctg ggc cct gag ttt      512
63 Leu Ser Ile Met Ser Gly Gln Pro Arg Ala Gln Leu Gly Pro Glu Phe
64           105         110         115
66 cga cag aat gaa gca gac ggc caa tgg agc ctt gtt att acg caa aga      560

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67	Arg	Gln	Asn	Glu	Ala	Asp	Gly	Gln	Trp	Ser	Leu	Val	Ile	Thr	Gln	Arg
68		120			125				130							
70	caa	gac	tac	gag	aca	gca	acc	atg	cag	agc	tat	gtg	ttc	tca	atc	caa
71	Gln	Asp	Tyr	Glu	Thr	Ala	Thr	Met	Gln	Ser	Tyr	Val	Phe	Ser	Ile	Gln
72		135			140				145							
74	gtg	gag	ggt	gaa	tca	cag	gcc	gta	ctg	gtg	gct	ctg	gag	ata	gtc	aac
75	Val	Glu	Gly	Glu	Ser	Gln	Ala	Val	Leu	Val	Ala	Leu	Glu	Ile	Val	Asn
76	150		155			160			165							
78	atc	gac	gac	aat	ccg	ccc	atc	ctg	caa	gtg	gtc	agc	gcc	tgc	gta	att
79	Ile	Asp	Asp	Asn	Pro	Pro	Ile	Leu	Gln	Val	Val	Ser	Ala	Cys	Val	Ile
80		170			175				180							
82	cca	gaa	cat	ggc	gag	gct	aga	ctg	acc	gac	tgc	gtg	tac	caa	gtg	tca
83	Pro	Glu	His	Gly	Glu	Ala	Arg	Leu	Thr	Asp	Cys	Val	Tyr	Gln	Val	Ser
84		185			190				195							
86	gac	cgc	gac	ggt	gaa	atc	agc	acc	cgc	ttc	atg	acg	ttc	cgt	gtc	gac
87	Asp	Arg	Asp	Gly	Glu	Ile	Ser	Thr	Arg	Phe	Met	Thr	Phe	Arg	Val	Asp
88		200			205				210							
90	agc	agc	agg	gct	gca	gat	gaa	agc	atc	ttc	tac	atg	gtt	gga	gaa	tac
91	Ser	Ser	Arg	Ala	Ala	Asp	Glu	Ser	Ile	Phe	Tyr	Met	Val	Gly	Glu	Tyr
92		215			220				225							
94	gac	ccc	agc	gac	tgg	ttc	aat	atg	aag	atg	act	gtg	ggg	atc	aat	tcg
95	Asp	Pro	Ser	Asp	Trp	Phe	Asn	Met	Lys	Met	Thr	Val	Gly	Ile	Asn	Ser
96		230			235				240				245			
98	ccc	ttg	aac	ttc	gag	aca	act	cag	ctt	cat	ata	ttt	agc	gtc	aca	gct
99	Pro	Leu	Asn	Phe	Glu	Thr	Thr	Gln	Leu	His	Ile	Phe	Ser	Val	Thr	Ala
100		250			255				260							
102	tct	gac	tcg	cta	ccg	aac	aac	cac	acg	gtc	acc	atg	atg	gtg	caa	gtg
103	Ser	Asp	Ser	Leu	Pro	Asn	Asn	His	Thr	Val	Thr	Met	Met	Val	Gln	Val
104		265			270				275							
106	gag	aac	gta	gag	tct	cg	ccc	cct	cg	tgg	gtg	gag	atc	ttc	tca	gtg
107	Glu	Asn	Val	Glu	Ser	Arg	Pro	Pro	Arg	Trp	Val	Glu	Ile	Phe	Ser	Val
108		280			285				290							
110	cag	cag	ttt	gac	gag	aag	act	aat	cag	agc	ttc	tcc	ctc	cgc	gct	ata
111	Gln	Gln	Phe	Asp	Glu	Lys	Thr	Asn	Gln	Ser	Phe	Ser	Leu	Arg	Ala	Ile
112		295			300				305							
114	gac	ggg	gac	acg	gga	atc	aat	agg	gcc	atc	aac	tat	acc	ctc	atc	agg
115	Asp	Gly	Asp	Thr	Gly	Ile	Asn	Arg	Ala	Ile	Asn	Tyr	Thr	Leu	Ile	Arg
116		310			315				320				325			
118	gat	gac	gct	gac	ttc	ttt	tcc	ctg	gag	gtg	att	gaa	gac	gga	gct	
119	Asp	Asp	Ala	Asp	Asp	Phe	Phe	Ser	Leu	Glu	Val	Ile	Glu	Asp	Gly	Ala
120		330			335				340							
122	att	ctg	cac	gtg	act	gag	atc	gac	cgc	gac	aag	ctt	gaa	aga	gag	ctt
123	Ile	Leu	His	Val	Thr	Glu	Ile	Asp	Arg	Asp	Lys	Leu	Glu	Arg	Glu	Leu
124		345			350				355							
126	ttc	aac	ctc	acc	atc	gtt	gct	tac	aaa	tct	act	gac	gct	agc	ttt	gca
127	Phe	Asn	Leu	Thr	Ile	Val	Ala	Tyr	Lys	Ser	Thr	Asp	Ala	Ser	Phe	Ala
128		360			365				370							
130	aca	gag	gcc	cac	att	ttc	atc	atc	gtc	aac	gac	gtc	aat	gat	cag	cga
131	Thr	Glu	Ala	His	Ile	Phe	Ile	Val	Asn	Asp	Val	Asn	Asp	Gln	Arg	

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132	375	380	385	
134	ccc gag ccg ctg cat aaa gaa tac agt att gat atc atg gag gaa act			1376
135	Pro Glu Pro Leu His Lys Glu Tyr Ser Ile Asp Ile Met Glu Glu Thr			
136	390	395	400	405
138	cca atg act cta aac ttc aat gaa gaa ttt gga ttc cat gat cga gat			1424
139	Pro Met Thr Leu Asn Phe Asn Glu Glu Phe Gly Phe His Asp Arg Asp			
140	410	415	420	
142	ttg ggt gaa aac gct caa tac aca gtg gaa ctt gag gac gtg ttc ccg			1472
143	Leu Gly Glu Asn Ala Gln Tyr Thr Val Glu Leu Glu Asp Val Phe Pro			
144	425	430	435	
146	cca ggg gcg gcg tcc gca ttc tac atc gcg ccg ggg agc ggc tac cag			1520
147	Pro Gly Ala Ala Ser Ala Phe Tyr Ile Ala Pro Gly Ser Gly Tyr Gln			
148	440	445	450	
150	agg cag acc ttc atc atg ggc acc ata aac cac acc atg ctg gat tac			1568
151	Arg Gln Thr Phe Ile Met Gly Thr Ile Asn His Thr Met Leu Asp Tyr			
152	455	460	465	
154	gaa gat gtc att ttt cag aac atc atc att aag gtc aaa gca gtg gac			1616
155	Glu Asp Val Ile Phe Gln Asn Ile Ile Lys Val Lys Ala Val Asp			
156	470	475	480	485
158	atg aac aac gct agc cac gtg ggc gag gcg ctg gtg tac gtg aac ctg			1664
159	Met Asn Asn Ala Ser His Val Gly Glu Ala Leu Val Tyr Val Asn Leu			
160	490	495	500	
162	atc aac tgg aac gac gaa ctt ccc atc ttc gag gag agc agc tac tcc			1712
163	Ile Asn Trp Asn Asp Glu Leu Pro Ile Phe Glu Glu Ser Ser Tyr Ser			
164	505	510	515	
166	gcg tcg ttt aag gag acc gtc ggc gcc ggc ttc ccg gtg gcc acg gtg			1760
167	Ala Ser Phe Lys Glu Thr Val Gly Ala Gly Phe Pro Val Ala Thr Val			
168	520	525	530	
170	ctc gcc ctc gac aga gac atc gac gac gta gta gtg cat tca ttg atg			1808
171	Leu Ala Leu Asp Arg Asp Ile Asp Asp Val Val Val His Ser Leu Met			
172	535	540	545	
174	ggc aac gct gtt gac tac ctg ttc ata gat gaa tca acg gga gag atc			1856
175	Gly Asn Ala Val Asp Tyr Leu Phe Ile Asp Glu Ser Thr Gly Glu Ile			
176	550	555	560	565
178	ttc gtg agc atg gac gat gcc ttc gac tac cac cga cag aac act cta			1904
179	Phe Val Ser Met Asp Asp Ala Phe Asp Tyr His Arg Gln Asn Thr Leu			
180	570	575	580	
182	ttt gtt cag gtg cgc gct gac gat act ttg ggc gac ggc cca cac aac			1952
183	Phe Val Gln Val Arg Ala Asp Asp Thr Leu Gly Asp Gly Pro His Asn			
184	585	590	595	
186	aca gtg acc acc cag ctg gtg ata gaa ctg gag gat gtc aac aac act			2000
187	Thr Val Thr Thr Gln Leu Val Ile Glu Leu Glu Asp Val Asn Asn Thr			
188	600	605	610	
190	cct ccc acc cta cgc ttg ccc cgt tcg act cca agc gtc gag gag aac			2048
191	Pro Pro Thr Leu Arg Leu Pro Arg Ser Thr Pro Ser Val Glu Glu Asn			
192	615	620	625	
194	gtt ccc gaa gga tac gag ata tcc cgg gaa atc act gct acc gac ccg			2096
195	Val Pro Glu Gly Tyr Glu Ile Ser Arg Glu Ile Thr Ala Thr Asp Pro			
196	630	635	640	645

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198 gac acc agc gcc tac ctg ttc gag atc gac tgg gac tcc acc tgg	2144
199 Asp Thr Ser Ala Tyr Leu Trp Phe Glu Ile Asp Trp Asp Ser Thr Trp	
200 650 655 660	
202 gcc acc aag cag ggc aga gag acc aac cct act gaa tac gtc ggg tgt	2192
203 Ala Thr Lys Gln Gly Arg Glu Thr Asn Pro Thr Glu Tyr Val Gly Cys	
204 665 670 675	
206 ata gtt atc gaa acg ata tac ccc acc gag ggc aac cgg ggt tcc gcc	2240
207 Ile Val Ile Glu Thr Ile Tyr Pro Thr Glu Gly Asn Arg Gly Ser Ala	
208 680 685 690	
210 atc ggg cgc ctc gtg gtg caa gag atc cgg gac aac gtc acc atc gac	2288
211 Ile Gly Arg Leu Val Val Gln Glu Ile Arg Asp Asn Val Thr Ile Asp	
212 695 700 705	
214 ttc gag gaa ttc gag atg ctt tac ctc acc gtc cgc gtg agg gac ctc	2336
215 Phe Glu Glu Phe Glu Met Leu Tyr Leu Thr Val Arg Val Arg Asp Leu	
216 710 715 720 725	
218 aac act gtc atc gga gat gac tac gat gag gcg acg ttc acg atc aca	2384
219 Asn Thr Val Ile Gly Asp Asp Tyr Asp Glu Ala Thr Phe Thr Ile Thr	
220 730 735 740	
222 ata atc gac atg aac gac aac gcg ccg atc ttc gcg aac ggc acg ctg	2432
223 Ile Ile Asp Met Asn Asp Asn Ala Pro Ile Phe Ala Asn Gly Thr Leu	
224 745 750 755	
226 acg cag acg atg cgc gtg cgc gag ctg gcg gcc acg ggc acg ctc atc	2480
227 Thr Gln Thr Met Arg Val Arg Glu Leu Ala Ala Ser Gly Thr Leu Ile	
228 760 765 770	
230 ggc tcc gtg ctc gcc acc gac atc gac ggc ccg ctc tac aac caa gtg	2528
231 Gly Ser Val Leu Ala Thr Asp Ile Asp Gly Pro Leu Tyr Asn Gln Val	
232 775 780 785	
234 cgc tac act ata caa cct aga aac aac act ccc gag gga tta gtg aag	2576
235 Arg Tyr Thr Ile Gln Pro Arg Asn Asn Thr Pro Glu Gly Leu Val Lys	
236 790 795 800 805	
238 att gac ttc aca act ggt caa att gag gtg gat gcg aac gag gcg atc	2624
239 Ile Asp Phe Thr Thr Gly Gln Ile Glu Val Asp Ala Asn Glu Ala Ile	
240 810 815 820	
242 gat gca gac gaa ccc tgg cgc ttc tac ttg tac tac acc gtc atc gct	2672
243 Asp Ala Asp Glu Pro Trp Arg Phe Tyr Leu Tyr Tyr Thr Val Ile Ala	
244 825 830 835	
246 gac gac gag tgc tcc ctg gaa aac cgc acg gaa tgt cct cca gat tcc	2720
247 Ser Asp Glu Cys Ser Leu Glu Asn Arg Thr Glu Cys Pro Pro Asp Ser	
248 840 845 850	
250 aac tac ttc gaa gtt cca ggc gat atc gaa ata gaa atc atc gac aca	2768
251 Asn Tyr Phe Glu Val Pro Gly Asp Ile Glu Ile Glu Ile Ile Asp Thr	
252 855 860 865	
254 aac aac aaa gtg cct gag ccg ctc act gag aag ttc aac acg acg gtg	2816
255 Asn Asn Lys Val Pro Glu Pro Leu Thr Glu Lys Phe Asn Thr Thr Val	
256 870 875 880 885	
258 tac gtc tgg gag aat gcc acg agc ggc gac gag gtg gtc cag ctg tac	2864
259 Tyr Val Trp Glu Asn Ala Thr Ser Gly Asp Glu Val Val Gln Leu Tyr	
260 890 895 900	
262 tcc cac gac cgt gac aga gac gag ttg tac cac acg gta,cga tac acg	2912

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263	Ser	His	Asp	Arg	Asp	Arg	Asp	Glu	Leu	Tyr	His	Thr	Val	Arg	Tyr	Thr	
264	905								910							915	
266	atg	aac	ttt	gcg	gtg	aac	ccc	cga	ctg	cg	gat	ttc	ttc	gag	gtg	gac	
267	Met	Asn	Phe	Ala	Val	Asn	Pro	Arg	Leu	Arg	Asp	Phe	Phe	Glu	Val	Asp	
268	920								925							930	
270	ctg	gac	act	ggt	cgc	ctt	gag	gtg	cat	tac	ccg	ggg	gac	gaa	aaa	ttg	
271	Leu	Asp	Thr	Gly	Arg	Leu	Glu	Val	His	Tyr	Pro	Gly	Asp	Glu	Lys	Leu	
272	935								940							945	
274	gac	cgc	gat	ggg	gat	gag	cct	aca	cat	act	atc	ttt	gta	aat	ttc	atc	
275	Asp	Arg	Asp	Gly	Asp	Glu	Pro	Thr	His	Thr	Ile	Phe	Val	Asn	Phe	Ile	
276	950								955							965	
278	gat	aac	ttc	ttt	tct	gat	gg	gtt	gac	gg	agg	aga	aac	cag	gac	gaa	gtt
279	Asp	Asn	Phe	Phe	Ser	Asp	Gly	Asp	Gly	Arg	Arg	Asn	Gln	Asp	Glu	Val	
280	970								975							980	
282	gaa	ata	ttt	gtc	gtt	cta	ttg	gat	gtg	aac	gac	aac	gct	cct	gag	atg	
283	Glu	Ile	Phe	Val	Val	Leu	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro	Glu	Met	
284	985								990							995	
286	cca	ttg	cct	gat	gaa	ctc	cg	ttt	gat	gtt	tcc	gaa	gga	gca	gtt	gt	
287	Pro	Leu	Pro	Asp	Glu	Leu	Arg	Phe	Asp	Val	Ser	Glu	Gly	Ala	Val	Ala	
288	1000							1005								1010	
290	gg	gt	gt	gt	ctc	cca	gaa	atc	tac	gca	ccg	gac	agg	gat	gaa	cca	
291	Gly	Val	Arg	Val	Leu	Pro	Glu	Ile	Tyr	Ala	Pro	Asp	Arg	Asp	Glu	Pro	
292	1015							1020								1025	
294	gac	acg	gac	aa	tcg	cgt	gtc	gg	tac	gga	atc	ctg	gac	ctc	acg	atc	
295	Asp	Thr	Asp	Asn	Ser	Arg	Val	Gly	Tyr	Gly	Ile	Leu	Asp	Leu	Thr	Ile	
296	1030							1035								1040	
298	acc	gac	cga	gac	atc	gag	gt	ccg	gat	ctc	ttc	acc	atg	atc	tcg	att	
299	Thr	Asp	Arg	Asp	Ile	Glu	Val	Pro	Asp	Leu	Phe	Thr	Met	Ile	Ser	Ile	
300	1050							1055								1060	
302	gaa	aa	aa	act	ggg	gaa	ctt	gag	acc	gct	atg	gac	ttg	agg	ggg	tat	
303	Glu	Asn	Lys	Thr	Gly	Glu	Leu	Glu	Thr	Ala	Met	Asp	Leu	Arg	Gly	Tyr	
304	1065							1070								1075	
306	tgg	ggc	act	tac	gaa	ata	ttc	att	gag	gcc	ttc	gac	cac	ggc	tac	ccg	
307	Trp	Gly	Thr	Tyr	Glu	Ile	Phe	Ile	Glu	Ala	Phe	Asp	His	Gly	Tyr	Pro	
308	1080							1085								1090	
310	cag	cag	agg	tcc	aa	cc	gag	ac	tg	acc	ctg	gtc	atc	cg	ccc	ttc	
311	Gln	Gln	Arg	Ser	Asn	Glu	Thr	Tyr	Thr	Leu	Val	Ile	Arg	Pro	Tyr	Asn	
312	1095							1100								1105	
314	ttc	cac	cac	cct	gt	ttc	gt	ttc	ccg	caa	ccc	gac	tcc	gtc	att	cg	
315	Phe	His	His	Pro	Val	Phe	Val	Phe	Pro	Gln	Pro	Asp	Ser	Val	Ile	Arg	
316	1110							1115								1120	
318	ctt	tct	agg	gg	ccg	gca	aca	gaa	ggc	ggc	gtt	ctg	g	ac	g	ct	
319	Leu	Ser	Arg	Glu	Arg	Ala	Thr	Glu	Gly	Val	Leu	Ala	Thr	Ala	Ala		
320	1130							1135								1140	
322	aac	gag	ttc	ctg	gag	ccg	atc	tac	g	cc	acc	gac	gag	ggc	ctc	cac	
323	Asn	Glu	Phe	Leu	Glu	Pro	Ile	Tyr	Ala	Thr	Asp	Glu	Asp	Gly	Leu	His	
324	1145							1150								1155	
326	g	cg	gg	ac	gt	ac	tg	cc	ac	gt	cc	g	at	g	g	tg	
327	Ala	Gly	Ser	Val	Thr	Phe	His	Val	Gln	Gly	Asn	Glu	Glu	Ala	Val	Gln	

VERIFICATION SUMMARY  
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L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date